REMARKS

Claims 1 to 107 have been canceled without prejudice to subsequent revival in this application or in one or more related applications. New claims 108 to 151 have been added. The new claims are presented for the purpose of advancing the case toward allowance and differences between the new claims and the previously pending claims should not be viewed as acquiescence to any of the Examiner's rejections. The new claims are believed to include no new matter.

The Examiner rejects the pending claims under 35 USC 112, first paragraph, as failing to comply with the written description requirement. First, the Examiner indicates that an insufficient number of species are presented in the application to support the genus of claimed nucleic acids. Applicant traverses the rejection.

The Examiner states that the claimed genus "encompasses potentially a large number of nucleic acid sequences of various structure and size that have sequence homology with SEQ ID NO:1 (75-100%) and/or SEQ ID NO:2, wherein such nucleic acid molecule[s] may not even be related to a gene expression controlling region." Applicant first submits that the claims include the functional limitation of "comprising a gene expression controlling region". Therefore, in fact, the nucleic acid molecules claimed must be related to a gene expression controlling region. With regard to the Examiner's assertion that the claims encompass a potentially large number of nucleic acid sequences, applicant reminds the Examiner that "The test for determining compliance with the written description requirement is whether the disclosure of the application as originally filed reasonably conveys to the artisan that the inventor had possession at the time of the later claimed subject matter, rather than the presence or absence of literal support in the specification for the claim language." See, In re Kaslow, 707 F.2d 1366, 1375. In further support of applicant's position, while not binding precedent, the Board of Patent Appeals and Interferences of the United States Patent and Trademark Office has found in recent decisions that the written description requirement is fulfilled for claims which are drawn to certain percent nucleotide sequence identities for defined nucleotide sequences. One such case is Ex parte Bandman et al (Bandman) (copy included with this amendment).

The facts in Bandman are quite similar to those in the present case. In Bandman, the applicant is claiming, among other things, "a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO: 4". In Bandman the Examiner states that one of skill in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time of filing since "The specification discloses only a single species of the claimed genus (i.e., the sequence encoding SEQ ID NO: 2) which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus." In the case the Board not only found that the written description requirement had been met, but that the requirement had been met even though the claim at issue did not include a functional limitation. Claims in the present case not only include a reference nucleotide sequence of the claimed genus, but also include a defined function which can be readily assayed for as discussed below. Therefore, applicant submits that claims in the present case relating to sequence identity

certainly meet the written description requirement.

The Examiner also states that the specification discloses that two fragments from the chicken iFABP gene (0.6 and 1.6 kb) that direct expression of the reporter gene in certain cell lines, whereas the 1.1 kb fragments fails to show promoter activity in the reporter assay and that the specification fails to teach whether the nucleic acid fragment of SEQ ID NO: 1 and SEQ ID NO: 2 have promoter activity.

Applicant disagrees with the Examiner because, for example, at page 39, line 32 to page 40, line 2 of the specification it is stated that "the proximal 0.5 kbp showed high promoter activity, while longer (1.1 and 1.6 kb) 5'-flanking sequences showed modest promoter activity." Therefore, the specification shows that the 1.1 kb fragment does have promoter activity. Additionally, applicant has shown that the proximal 0.5 kb fragment possesses high promoter activity. The 0.5 kb fragment and the 0.3 kb fragment (SEQ ID NO: 2) begin upstream of the transcription start site with the 0.3 kb fragment encompassed by the 0.5 kb fragment. And, as disclosed in the specification, at page 4, lines 3 to 8: "Several elements in the proximal 0.3 kb region have been nominated as regulatory sequences involved in tissue specific expression of iFABP, particularly in the rat. For example, a 14-bp element composed of two direct 7-bp repeats is conserved among the gene promoters of several small intestine-specific genes in mammals. Two members of the steroid hormone receptor superfamily, HNF-4 and ARP-1 are reported to bind to the iFABP promoter element (Issemann and Green, 1990; Rottman and Gordon, 1993)." Therefore, applicant submits that a skilled artisan would reasonably expect that the 0.3 kb sub-sequence of the 0.5 kb sequence comprises a gene expression controlling activity (e.g., promoter activity).

The Examiner also states that the claimed genus of nucleic acid molecules drawn to nucleotide sequences which hybridize to SEQ ID NO:1 or SEQ ID NO:2 is potentially large and is represented only by SEQ ID NO:1 and SEQ ID NO:2.

Applicant submits that claiming nucleic acid molecules by hybridization is an accepted practice recognized in recent decisions of the United States Court of Appeals for the Federal Circuit. For example, in Enzo v Genprobe (296 F.3d at 1324) (Enzo) guidelines for claiming nucleic acid molecules by hybridization are described by the court. In the case the claims at issue provided no sequence information and the court finds that where hybridization "is the only characteristic purportedly describing the claimed nucleotide sequences" the written description requirement is not satisfied. The court summarizes their ruling on the issue by stating that "in the absence of sequence information for its hybridization site, a nucleic acid described only by its ability to hybridize with another DNA fails to meet the description of § 112, ¶ 1." Clearly, the present claims comply with this standard suggested by the Court of Appeals since, in addition to functional requirement, sequence information is provided (e.g., SEQ ID NO: 67) in the claims. Therefore, applicant submits that claims in the present case relating to hybridization meet the written description requirement.

The Examiner states that the specification fails to disclose elements(s)/structures(s)/sequences(s) that the claimed fragments must share for the promoter or

gene expression function. Applicant submits that there is no requirement to specifically point out those elements(s)/structures(s)/sequences(s) within a sequence required for promoter activity. However, the application does in fact point out a TATA box like element (see, description of Fig. 2). Other putative gene expression controlling regions could readily be identified at the time of filing utilizing computer software programs. Whether or not such elements(s)/structures(s)/sequences(s) contained within SEQ ID NO:1 (and therefore, within SEQ ID NO:2) were specifically identified before filing is irrelevant as to whether applicant was in possession of the invention as claimed.

In summary, applicant has shown that the claims comply with the written description requirement of 35 USC 112, first paragraph.

The Examiner rejects certain of the claims under 35 USC 112, first paragraph, as not being enabling in a host cell in vivo. Applicant traverses the rejection. However, applicant submits herein new claims which applicant believes obviate the Examiner's rejection.

The Examiner rejects certain of the claims under 35 USC 112, second paragraph, as being indefinite for failing to distinctly claim the subject matter which applicant regards as the invention. Applicant traverses the rejection.

The Examiner states that it appears to be redundant to recite "the complement" in the claims. In particular, the Examiner states that a nucleic acid having homology to SEQ ID NO:1/SEQ ID NO:2 would have homology with the complementary sequence and that a nucleic acid that hybridizes to the sequence of SEQ ID NO:1/SEQ ID NO:2 would also hybridize to its complementary sequence.

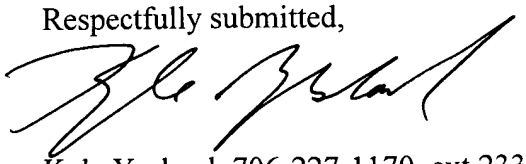
Applicant disagrees with the Examiner because, for example, it is well known that a complement to a first single stranded nucleotide sequence (first sequence) is a sequence that when positioned diametrically to the "first sequence" will have a purine nucleotide at each position where a pyrimidine nucleotide is present in the "first sequence" and will have a pyrimidine nucleotide present at each position where a purine nucleotide is present in the "first sequence." That is, for each position where a guanosine is present in the "first sequence" a cytosine will be present in the complement and for each position where a cytosine is present in the "first sequence" a guanosine will be present in the complement and for each position where an adenosine is present in the "first sequence" a thymidine will be present in the complement and for each position where a thymidine is present in the "first sequence" an adenosine will be present in the complement. Therefore, it can be seen that a nucleotide sequence that has homology to a certain nucleotide sequence would not be expected to have homology to the complement of the certain nucleotide sequence and a nucleotide sequence that hybridizes to a certain nucleotide sequence would not be expected to hybridize to the complement of the certain nucleotide sequence.

The Examiner also rejects certain claims which contain certain recitations such as "derived", "a gene expression controlling region...further comprises a nucleotide sequence encoding a polypeptide", "a codon complement optimized for protein expression..." and "a gene expression controlling region further comprising a vector". Applicant submits herein new claims which

applicant believes obviate certain aspects of the Examiner's rejection.

If any issues remain to be addressed in this matter, which might be resolved by discussion, the Examiner is respectfully requested to call applicants' undersigned counsel at the number indicated below.

Respectfully submitted,



Kyle Yesland, 706-227-1170, ext 233
Attorney for Applicants
Reg. No. 45,526
AviGenics, Inc.
111 Riverbend Rd.
Legal Department
Athens, Georgia 30605